Figure 1

SEQ ID NO:1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV	60
VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG	120
ADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF	180
LNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC	227

SEQ ID NO:2

DEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFP	60
GAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPP	120
AHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQD	180
SPTLQAPRERASEPKHKNQAEIAAC	205

SEQ ID NO:3

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV	60
VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG	120
ADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF	180
LNRFHLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRRR	223

SEQ ID NO:4

DEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFP	60
GAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPP	120
AHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQD	180
SPTLQAPRGRASEPKHKTRRR	201

SEQ ID NO:5

ITSWMEPIVK	10

SEQ ID NO:6

FPGAVDGATYILVMVDPDAPSR	22

SEQ ID NO:7

HWLVTDIK	8

SEQ ID NO:8

IQGQELSAYQAPSPPAHSGFHR	22

SEQ ID NO:9

YQFFVYLQEGK	11

SEQ ID NO:10

VISLLPK	7

Figure 2

CLUSTAL W (1.81) multiple sequence alignment

```
PEBP_HUMAN      ------PVDLSKWSGPLSLQEVDEQPQHP--------------------LHVTYAGAAVDELGK
PEBP_BOVIN      ------PVDLSKWSGPLSLQEVDERPQHP--------------------LQVKYGGAEVDELGK
Q96S96          MGWTMRLVTAALLGLMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYP--ELGNIGC
                      *  :  **  : :    * *   *   *   * *:*:  ::  :*

PEBP_HUMAN      VLTPTQVKNRPTSISWDG-------LDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNM
PEBP_BOVIN      VLTPTQVKNRPTSITWDG-------LDPGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNM
Q96S96          KVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDI
                 :  :  . :  * :   .     *  **:.* * *  *:*:****: :*. ::

PEBP_HUMAN      KGNDISSG----TVLSDYVGSGPPKGTGLHRYVWLVYEQDRPLKCDEPILSNRSGDHRGK
PEBP_BOVIN      KGNNISSG----TVLSDYVGSGPPKGTGLHRYVWLVYEQEGPLKCDEPILSNRSGDHRGK
Q96S96          KGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVIS----LLPKENKTRGS
                **  :  *    **:**  ...** .*:***  ::*:**:*  :  :    *  :.  .*.

PEBP_HUMAN      FKVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSGK-------------
PEBP_BOVIN      FKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSGK-------------
Q96S96          WKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC
                :*: .**:.::  *  .:  : . : :.  * *    *.:
```

Figure 3

CLUSTAL W (1.81) multiple sequence alignment

```
Q9D9G2    --MTMKLVAAALCLRLLAAGLWVGLSLTAESIEEGKPGGEKPGGGKPGGSGRGCFLPPLP
Q9D9L9    --MTMKLVAAALCLSLLAAGLWVGLSLTAESIEEGKPGGEKPGGGKPGGSGRGCFLPPLP
Q96S96    MGWTMRLVTAALLLGLMMV------VTGD-EDENSP-------------------CAHEALL
Q8WW74    MGWTMRLVTAALLLGLMMV------VTGD-EDENSP-------------------CAHEALL
               **:.:**.*** *:  .          *       .             .*   .  *

Q9D9G2    KEDVSLCRNLEVFYMEMGNISCKIVPKCNLYRQKIPAWQAPIVKFHTALDGALYLLVMVD
Q9D9L9    KEDVSLCRNLEVFYMEMGNISCKIVPKCNLYRQKITAWQAPIVKFHTALD---------
Q96S96    DEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVD
Q8WW74    DEDTLFCQGLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVD
           .* .:.**:* * *  *:*** * **.** .:* **:  *:.*   * *****

Q9D9G2    PDAPSRSNPVMKYWRHWLVSNITGADMKSGSIRGNVLSDYSPPTPPPETGVHRYQFFVYL
Q9D9L9    ----------------------VS------ELGWLKENVGP-----------------
Q96S96    PDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYL
Q8WW74    PDAPSRAEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYL
           ******       .*******  ***:*   *         *     *  ********

Q9D9G2    QGDRDISLSVEEKANLGGWNLDKFLQQYGLRDPDTSTQFMTQFDEELSSEFGRINDDQEQ
Q9D9L9    ----------------------------------------------------------
Q96S96    QEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEP
Q8WW74    QEGKVISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRGRASEP
           * *  **     * * *   ***     *      ****   *  *

Q9D9G2    FNQK----
Q9D9L9    --------
Q96S96    KHKNQAEIAAC
Q8WW74    KHKTRRR----
                   *
```

Figure 4